Interleukin-21

1	GGCACGAGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCT	60
1	ARVDTDEDRYPQKLAFAECL Domain II	20
61	GTGCAGAGGCTGTATCGATGCACGGACGGCCGCGAGACAGCTGCGCTCAACTCCGTGCG	120
21	CRGCIDARTGRETAALNSVR Domain II	40
121	GCTGCTCCAGAGCCTGCTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT	180
41	L L Q S L <u>L V L R R P</u> C S R D G S G L Domain III	60
181	CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCAC	240
61	PTPGAFAFHTEFIH <u>VPVGCT</u> Domain IV	80
241		300
81 <i>Dc</i>		87
301	GTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATT	360
361	AACACTACCCTTGGGGTCTGGGGCATTCCCCGTGTCTGGAGGACAGCCCCCCACTGTTCTC	420
421	ĆTCATCTCCAGCCTCAGTAGTTGGGGGTWGAAGGAGCTCAGCACCTCTTCCAGCCCTTAA 	480
481	AGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGGCT	540
541	TCCCTTACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGA	600
601	AGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAACAC	660
661	ΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑ	

FIG. 1

2/13 Interleukin-22

			•				•			•			•				•			7.	
1	GGAA	TTC	:GGC	ACG	AGC	TCG	TGC	CGT	GCT	CAG	TGC	CTT	CCA	.CCA	CAC	GCT	GCA	GCT	GGG	GĊ 🗽	-60
1	N	S	A	R	Α	R	A	V	L	S	Α	F	Н	Н	T	L	Q	L	G	P	20
						#	•														
61	CGCG	TGA	.GCA	.GGC	GCG	CAA	CGC	GAG	CTG	CCC	GGC	AGG	GGG	CAG	GCC	CGC	CGA	CCG	CCG	CT	120
21	R	E	Q	A	R	N	Α	S	С	P	Α	G	G	R	P	Α	D	R	R	F	40
121	TCCG	GCC	GCC	CAC	CAA	CCT	GCG	CAG	CGT	GTC	GCC	CTG	GGC	СТА	CAG	AAT	CTC	СТА	CGA	CC	180
41	R	P	P	T	N	L	R	S	V	S	P	W	Α	Y	R	Ι	S	Y	D	P	60
																		Don	ain	I	
																				•	
181	CGGC	GAG	GTA	CCC	CAG	GTA	CCT	GCC	TGA	AGC	CTA	CTG	CCT	GTG	CCG	GGG	CTG	CCT	GAC	CG	240
61	A			<u>P</u>	R	Y	L	Р	E	A	Y	<u>C</u>	L		R	G	<u>C</u>	L	T	G	80
	I	Doma	iin	Ι										Dom	ain	II					
			•							•			•				•			•	
241	GGCT																				300
81	L	F	G	E	Ε	D	V	R	F	R	S	A	P	V	Y	M	Р		<u>^</u>	_	100
																		DOM	aın	III	
201	maam			C 3 C	000	aaa	ama	aaa	aaa		aaa	mmø	~~m		an a	CON	aaa	OM 3	aam.	(7)	260
301 101	TCCT	GCG R		-	CCC P	CGC A	-	JUJ A		CGG G	CCG R	S	V V	СІА Ү	CAC T	CGA E	JUU A	CIA Y	V V	СA T	360 120
101		oma Doma				А	C	А	G	G	Л	5	V	1	1	Ŀ	А	I	V	1	120
	L	Ollia	1111	111															#		
361	CCAT	יכככ	ርርጥ	GGG	ርፐር	CAC	· ሮፐር	ርርT	רככ	· CGA	GCC	GGA	Gaa	GGA	ርርር	AGA	· CAG	САТ	" ("A A:	· CT	420
121	I		V		C	Т	C	V	P	E	P	E	K	D	A	D	S	Ι	N	S	140
	-		I	oma	iin	ĪV						_		_		_	_	_		_	
							•														
421	CCAG	САТ	CGA	CAA	ACA	GGG	CGC	CAA	GCT	CCT	GCT	GGG	CCC	CAA	CGA	CGC	GCC	CGC	TGG	CC	480
141	S	Ι	D	K	Q	G	Α	K	L	L	L	G	P	N	D	Α	Р	Α	G	P	160
481	CCTG	AGG	CCG	GTC	CTG	CCC	CGG	GAG	GTC'	TCC	CCG	GCC	CGC.	ATC	CCG.	AGG	CGC	CCA	AGC'	TG	540
541	GAGC	CGC	CTG	GAG	GGC	TCG	GTC	GGC	GAC	CTC	TGA	AGA	GAG	TGC.	ACC	GAG	CAA	ACC.	AAG	TG	600
601	CCGG	AGC.	ACC.	AGC	GCC	GCC'	TTT	CCA'	TGG.	AGA	CTC	GTA	AGC.	AGC'	TTC.	ATC'	TGA	CAC	GGG	CA	660

FIG. 2A

3/13 Interleukin-22

661	TCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACC	2720a
721	$. \\ CGGCACGGGCATCCTGTGTGCGGCCCGCATGGAGGGTTTGGAAAAGTTCACGGAGGCTCC$	780
781		840
841	GCCAAAGAGATAGGGACGCATATGCTTTTTAAAGCAATCTAAAAATAATAATAAGTATAG	900
901	CGACTATATACCTACTTTTAAAATCAACTGTTTTGAATAGAGGCAGAGCTATTTTATATT	960
961	ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTTACTTCTTC	1020
1021	TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTC	1080
1081	TGGCCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGA	1140
1141	CATCTGACCCACTCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG	1200
1201	ATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGG	1260
1261	TTTTAGTCATGAATACATAAACAGTCTCAAACTCGCACAATTTTTTCCCCCTTTTGAAAG	1320
1321	CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGAACGTGACATCTTT	1380
1381	GCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG	1440
1441	CTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT	1500
1501	GTTTCTGCATTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGT	1560
1561	CTCTGAACACAATTATTTGTAAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTT	1620
1621	GCTGAAAAAAAAAAAAAA 1642	

FIG. 2B

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IL-17.aa VIL-17.aa IL20.aa IL-21.aa IL-21.aa IL-22.aa	. II-17.aa MII-17.aa VII-17.aa II-21.aa II-22.aa II-22.aa II-22.aa
40 50 1 1 P R N P G C P N S E D	90 100 100 100 100 100 100 100 100 100 1
30EAIVKAGIAATVKAAADCIVKSEI QPRSPKSKRKG	M V N L N L - H N R N K V N L K V F N S L G M N N N N N N N N N N N N N N N N N N
10 20 20	60 70
MT PGKT SLV MSPGRASSV MTFRMTSLV MDWPHNLLF A	S R M K P Y A R M J P P - H L L A R G Z Q L Y G R
FIC	G. 3A

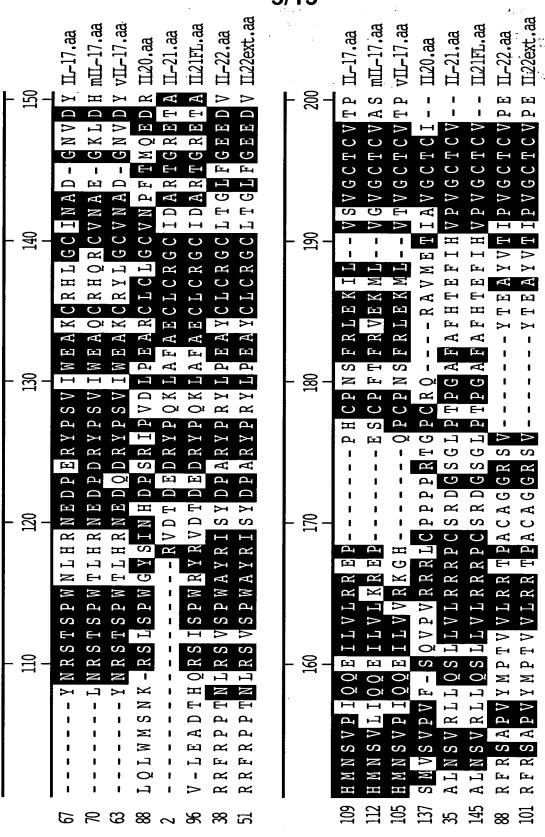
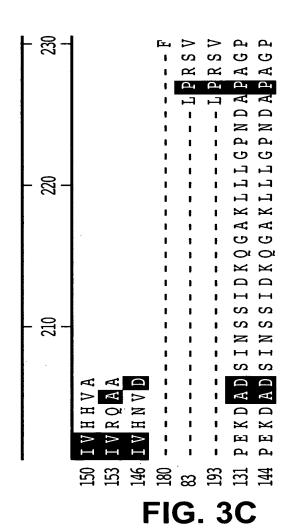
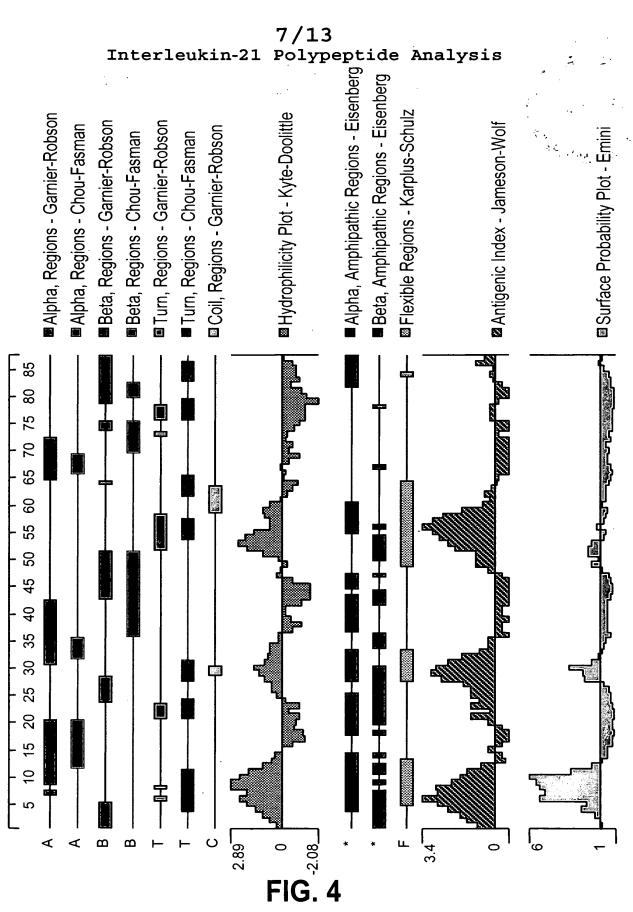


FIG. 3B

IL-17.aa mIL-17.aa vIL-17.aa II-21.aa II-21.aa II-22.aa II-22.aa



Interleukin-21



■ Hydrophilicity Plot - Kyte-Doolittle

Alpha, Amphipathic Regions - Eisenberg and Beta, Amphipathic Regions - Eisenberg and Flexible Regions - Karplus-Schulz

Anticenic Index - Jameson-Wolf Interleukin-22 Alpha, Regions - Garnier-Robson Beta, Regions - Garnier-Robson ■ Turn, Regions - Garnier-Robson Antigenic Index - Jameson-Wolf Alpha, Regions - Chou-Fasman ☐ Coil, Regions - Garnier-Robson ■ Turn, Regions - Chou-Fasman ■Beta, Regions - Chou-Fasman Surface Probability Plot - Emir 140 120 100 8 9 40 20 ပ Ф ⋖ Ω ၑ

FIG. 5

Interleukin-21

		•
1	GCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCC	TGTTT
1	MTLLPGLL	<u>F</u>
	•	
61		CCCAC
10	<u>L T W L H T C L A</u> H H D P S L R G H P	Н
	·	
121	AGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCC	CCCCA
30		P
	Domain V	
	•	
181		CCAGC
50	H L L A R G A K W G Q A L <u>P V A L V S</u>	S
	Domain VI	
		•
241		GCCCG
70	L E A A S H R G R H E R P S A T T Q C	P
	• • • • • • • • • • • • • • • • • • • •	•
301		CCTGG
90		W
	Domain VII	
	• • • • • • • • • • • • • • • • • • • •	•
361		
110	R Y R <u>V D T D E D R Y P</u> Q K L A F A E	<u>C</u>
	Domain I	Domai
40.5		
421	CTGTGCAGAGGCTGTATCGATGCACGGACGGCCGCGAGACAGCTGCGCTCAACT	
130	L C R G C I D A R T G R E T A A L N S	V
	Domain II	
407		
481		
150		G
	Domain III	
г <i>и</i> л		
	CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCG	
170		
	Domair	1 1V

FIG. 6A

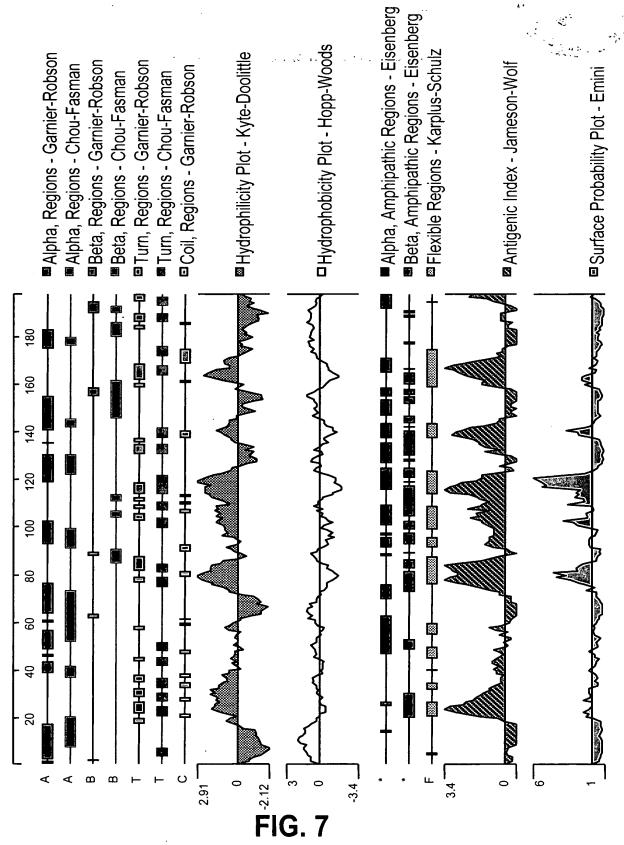
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Interleukin-21

601 190	ACCTGCGTGCCCCGTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC T C V L P R S V Domain IV	660 197
•		
661	GTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATT	720
721	CCAACACTACCCTTGGGGTCTGGGGCATTCCCCGTGTCTGGAGGACAGCCCCCCACTGTTC	780
781		840
841	AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGG	900
901	CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG	960
961	GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC	1020
1021		

FIG. 6B

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Interleukin-21 Polypeptide Analysis



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Interleukin-22

			•																	
GG	CTO	GCGC	CGGI	ACCO	GC(CGGI	AGG <i>I</i>	AGC'I	CAC'	rgg <i>i</i>	AGCI	\GC1	rgt <i>a</i>	ACGO	GCC	CCI	'GGC	:GGC	CCGGC	
G	С	Α	D	R	P	Е	E	L	L	Ε	Q	L	Y	G	R	L	Α	Α	G	
							1											#	_	
GT	'GC'I	'CAG	TGC	CTT	CCF	ACCA	ACAC	CGCT	:GC#	AGCT	GGG	GCC	CGCG	TGA	\GCA	GGC	GCC:		CGCG	
_									~		_				~					
AG	CTG	CCC	:GGC	'AGG	GGG	CAC	GCC	CCGC	CCGF	ACCG	CCG	CTT	CCG	GCC	:GCC	CAC	CAA	CCI	'GCGC	
													R	Р			N	L	R	
AG	CGT	'GTC	:GCC	CTG	GGC	CTA	CAC	:AAT	CTC	CTA	CGA	CCC	:GGC	'GAC	GTA	CCC	CAG	GTA	CCTG	
								_												
CC	TGA	AGC	CTA	CTG	CCI	GTO	CCG	GGG	CTO	CCT	'GAC	'CGG	GCT	'GTT	'CGG	CGA	.GGA	.GGA	CGTG	
P	E	A	Y	С	L	С	R	G	С	L	Т	G	L	F	G	E	Е	D	V	
					C.	D-I	I													
CG	CTT	CCG	CAG	CGC	CCC	TGT	'CTA	CAT	'GCC	CAC	CGT	'CGT	'CCT	GCG	CCG	CAC	CCC	CGC	CTGC	
R	F	R	S	Α	P	V	Y	M	P	T	V	V	L	R	R	Т	P	Α	С	
													C	D-I	ΙΙ					
GC	CGG	CGG	CCG	TTC	CGT	'CTA	CAC	CGA	.GGC	СТА	CGT	'CAC	CAT	CCC	CGT	GGG	CTG	CAC	CTGC	
A	G	G	R	S	V	Y	T	E	Α	Y	V	T	Ι	P	V	G	С	T	С	
																CD-	IV			
											#									
GT	CCC	CGA	GCC	GGA	GAA	GGA	.CGC	AGA	.CAG	CAT	CAA	.CTC	CAG	CAT	CGA	CAA	ACA	GGG	CGCC	
V	P	Ε	P	E	K	D	Α	D	S	Ι	N	S	S	Ι	D	K	0	G	Α	
D-I1	7																_			
AA	GCT	ССТ	GCT	GGG	CCC	CAA	.CGA	.CGC	GCC	CGC	TGG	CCC	CTG	Α	522					
	G GT V CD AG S GC A GT V AAA	G C GTGCT V L CD-VI AGCTG S C AGCGT S V CD-T CCTGA P E CGCTT R F GCCGG A G GTCCC V P D-IV AAGCT	G C A GTGCTCAG V L S CD-VI AGCTGCCC S C P AGCGTGTC S V S CD-VII CCTGAAGC P E A CGCTTCCG R F R GCCGGCGG A G G GTCCCCGA V P E D-IV AAGCTCCT	G C A D GTGCTCAGTGC V L S A CD-VI AGCTGCCCGGC S C P A AGCGTGTCGCC S V S P CD-VII CCTGAAGCCTA P E A Y CGCTTCCGCAG R F R S GCCGGCGGCCG A G G R GTCCCCGAGCC V P E P D-IV AAGCTCCTGCT	G C A D R GTGCTCAGTGCCTT V L S A F CD-VI AGCTGCCCGGCAGG S C P A G AGCGTGTCGCCCTG S V S P W CD-VII CCTGAAGCCTACTG P E A Y C CGCTTCCGCAGCGC R F R S A GCCGGCGGCGCCTTC A G G R S GTCCCCGAGCCGGA V P E P E D-IV AAGCTCCTGCTGGGG	G C A D R P GTGCTCAGTGCCTTCCA V L S A F H CD-VI AGCTGCCCGGCAGGGGG S C P A G G AGCGTGTCGCCCTGGGC S V S P W A CD-VII CCTGAAGCCTACTGCCT P E A Y C L CGCTTCCGCAGCGCCCC R F R S A P GCCGGCGGCGGCCGTTCCGT A G G R S V GTCCCCGAGCCGGGAGAA V P E P E K D-IV AAGCTCCTGCTGCCCTTCCAT A G G R S V AAGCTCCTGCTGGGCCCCC A G G R S V	G C A D R P E GTGCTCAGTGCCTTCCACCA V L S A F H H CD-VI AGCTGCCCGGCAGGGGGCAC S C P A G G R AGCGTGTCGCCCTGGGCCTA S V S P W A Y CD-VII CCTGAAGCCTACTGCCTGTC P E A Y C L C CD-I CGCTTCCGCAGCGCCCTGT R F R S A P V GCCGGCGGCGGCCCTT A G G R S V Y GTCCCCGAGCCGCGAGAAGGA V P E P E K D D-IV AAGCTCCTGCTGCTGGGCCCAA	G C A D R P E E GTGCTCAGTGCCTTCCACCACAC V L S A F H H T CD-VI AGCTGCCCGGCAGGGGGCAGGCC S C P A G G R P AGCGTGTCGCCTGCCCTGGGCCTACAC S V S P W A Y R CD-VII CCTGAAGCCTACTGCCTGTGCCC P E A Y C L C R CD-II CGCTTCCGCAGCGCCCCTGTCTA R F R S A P V Y GCCGGCGGGGGCCGTTCCGTCTACAC A G G R S V Y T GTCCCCGAGCCGGAGAAGGACGC V P E P E K D A D-IV AAGCTCCTGCTGCTGGGCCCCAACGA	G C A D R P E E L GTGCTCAGTGCCTTCCACCACACGCT V L S A F H H T L CD-VI AGCTGCCCGGCAGGGGGCAGGCCCGC S C P A G G R P A AGCGTGTCGCCTGGGCCTACAGAAT S V S P W A Y R I CD-VII CCTGAAGCCTACTGCCTGTGCCGGGG P E A Y C L C R G CD-II CGCTTCCGCAGCGCCCCTGTCTACAT R F R S A P V Y M GCCGGCGGCGCCCTTCCTACACGAA A G G R S V Y T E GTCCCCGAGCCGCGGAGAAGGACGCAGA V P E P E K D A D D-IV AAGCTCCTGCTGCTGGCCCAACGACGC	G C A D R P E E L L GTGCTCAGTGCCTTCCACCACACGCTGCA V L S A F H H T L Q CD-VI AGCTGCCCGGCAGGGGGGCCCGCCGA S C P A G G R P A D AGCGTGTCGCCCTGGGCCTACAGAATCTC S V S P W A Y R I S CD-VII CCTGAAGCCTACTGCCTGTGCCGGGGCTC P E A Y C L C R G C CD-II CGCTTCCGCAGCGCCCCTGTCTACATGCC R F R S A P V Y M P GCCGGCGGCGCCTTCCGTCTACACCGAGGC A G G R S V Y T E A GTCCCCGAGCCGCGGAGAAGGACGCAGACAG V P E P E K D A D S D-IV AAGCTCCTGCTGGGCCCCAACGACGCGCCC	G C A D R P E E L L E GTGCTCAGTGCCTTCCACCACACGCTGCAGCT V L S A F H H T L Q L CD-VI AGCTGCCCGGCAGGGGGGCAGGCCCGCCGACCG S C P A G G R P A D R AGCGTGTCGCCCTGGGCCTACAGAATCTCCTA S V S P W A Y R I S Y CD-VII CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCT P E A Y C L C R G C L CD-II CGCTTCCGCAGCGCCCCTGTCTACATGCCCAC R F R S A P V Y M P T GCCGGCGGCGCCGTTCCGTCTACACGAGGCCTA A G G R S V Y T E A Y GTCCCCGAGCCGGGGAGAAGGACAGCAT V P E P E K D A D S I D-IV AAGCTCCTGCTGGGCCCACGACGCCCCGCCCCCCCCCC	G C A D R P E E L L E Q GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGC V L S A F H H T L Q L G CD-VI AGCTGCCCGGCAGGGGGGCAGGCCCGCCGACCGCCG S C P A G G R P A D R R AGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGA S V S P W A Y R I S Y D CD-VII CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGAC P E A Y C L C R G C L T CD-II CGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGT R F R S A P V Y M P T V GCCGGCGGCGCCCTTCCGTCTACACCGAGGCCTACGT A G G R S V Y T E A Y V GTCCCCGAGCCGCGGAGAAGGACAGCATCAA V P E P E K D A D S I N D-IV AAGCTCCTGCTGGGCCCCACCACGACGCCCCGCTGGCCACCGTGGCCCCCCTGGGCCCCCCTGGGCCCCCCTGGGCCCCCC	G C A D R P E E L L E Q L GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCC V L S A F H H T L Q L G P CD-VI AGCTGCCCGGCAGGGGGCCGCCGCCGCCGCCGCCGCTT S C P A G G R P A D R R F AGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCC S V S P W A Y R I S Y D P CD-VII CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGG P E A Y C L C R G C L T G CD-II CGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGT R F R S A P V Y M P T V V GCCGGCGGCGCCGTTCCGTCTACACCGAGGCCTACGTCAC A G G R S V Y T E A Y V T GTCCCCGAGCCGGAGAAAGGACGCAGCATCAACTC V P E P E K D A D S I N S D-IV AAGCTCCTGCTGGGCCCCAACGACGCCCCCGCTGGCCC	G C A D R P E E L L E Q L Y GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGC V L S A F H H T L Q L G P R CD-VI AGCTGCCCGGCAGGGGGCCGCGCCGCCGCCGCCGCTTCCG S C P A G G R P A D R R F R AGCGTCTCGCCTGGGCCTACAGAATCTCCTACGACCCGGC S V S P W A Y R I S Y D P A CD-VII	G C A D R P E E L L E Q L Y G GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGGCGTGA V L S A F H H T L Q L G P R E CD-VI AGCTGCCCGGCAGGGGGCCAGGCCCGCCGCCGCCGCTTCCGGCC S C P A G G R P A D R R F R P AGCGTGTCGCCTGGGCCTACAGAATCTCCTACGACCCGGCGAG S V S P W A Y R I S Y D P A R CD-VII CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTT P E A Y C L C R G C L T G L F CD-II CGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCCTGCG R F R S A P V Y M P T V V L R CD-I GCCGGCGGCGCTTCCGTCTACACCGAGGCCTACGTCACCATCCC A G G R S V Y T E A Y V T I P GTCCCCGAGCCGCGGAGAAGGACAGCATCAACTCCAGCAT V P E P E K D A D S I N S S I D-IV AAGCTCCTGCTGGGCCCCAACGACGCCCCGCCCCTGA	G C A D R P E E L L E Q L Y G R GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCA V L S A F H H T L Q L G P R E Q CD-VI AGCTGCCCGGCAGGGGGCAGGCCCGCCGACCGCCGCTTCCGGCCGC S C P A G G R P A D R R F R P P AGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTA S V S P W A Y R I S Y D P A R Y CD-VII	G C A D R P E E L L E Q L Y G R L GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGC V L S A F H H T L Q L G P R E Q A CD-VI AGCTGCCCGGCAGGGGGCAGGCCCGCCGACCGCCGCTCCGGCCGCCAC S C P A G G R P A D R R F R P P T AGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTACCC S V S P W A Y R I S Y D P A R Y P CD-VII	GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGC VLLSAAFHHTLLQLGAACCGCGCGCGCGCGCGCCGCCCACCAA SCD-VI AGCTGCCCGGCAGGGGGCCGCCGCCGCCGCCGCCCCCCCC	G C A D R P E E L L E Q L Y G R L A A CD- GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCTGAGCAGGCGGCGCCAA V L S A F H H T L Q L G P R E Q A R N CD-VI AGCTGCCCGGCAGGGGGCCCGCCGACCGCCGCTCCGGCCGCCACCACCACCT S C P A G G R P A D R R F R P P T N L AGCTGCCCTGGCCTTGCGCCTACAGAATCTCCTACGACCCGGCGAGGTACCCCAGGTA S V S P W A Y R I S Y D P A R Y P R Y CD-VI CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGCGTTTCGGCGAGGAGGAA P E A Y C L C R G C L T G L F G E E D CD-II CGCTTCCGCAGCGCCCTGTCTACAATGCCCACCGTCGTCCTGCGCCGCACCCCCGC R F R S A P V Y M P T V V L R R T P A CD-III GCCGGCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGCTGCACC A G G R S V Y T E A Y V T I P V G C T CD-IV AAGCTCCTGGGCCCGAGGAAGGACGCAGCACGACACCTCAACAAACA	CD-VI

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Interleukin-22 Polypeptide Analysis

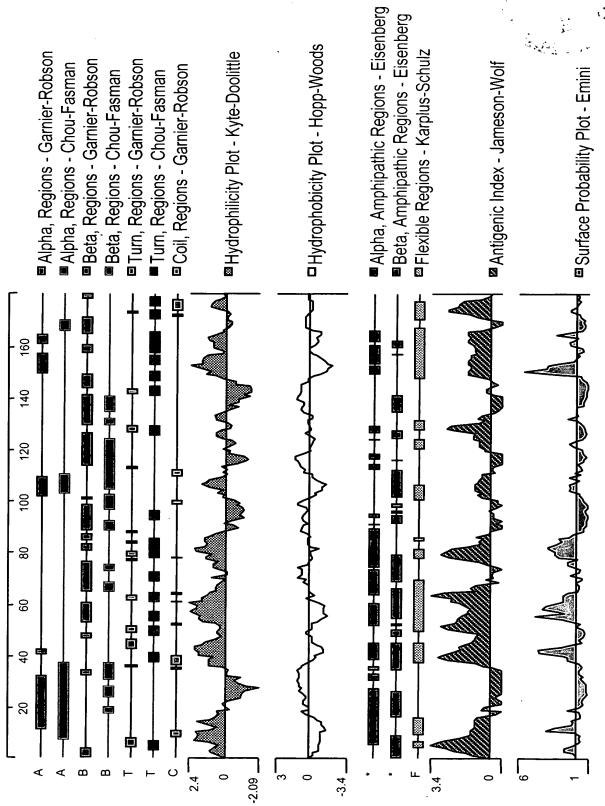


FIG. 9